

1 CGAGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTGTCCAGTGT
-----+-----+-----+-----+-----+-----+
61 AGATGAAC TCA TGA CTGTACTCTACCAGAA TATTGAA AATGTACAAGTGT CAGCTAAG
-----+-----+-----+-----+-----+-----+
M T V L Y P E Y W K M Y K C Q L R
-----+-----+-----+-----+-----+-----+
121 GAAAGAGGCTGGCAACATAACAGAGAACAGCCAACTCACTCAAGGACAGAGAGAC
-----+-----+-----+-----+-----+-----+
K G G W Q H N R E Q A N L N S R T E E T
-----+-----+-----+-----+-----+-----+
181 TATAAAATTTCCTGCAGCACATTATAATACAGAGATCTTGAAAGTATTGATTAATGAGTG
-----+-----+-----+-----+-----+-----+
I K F A A A H Y N T E I L K S I D N E W
-----+-----+-----+-----+-----+-----+
241 GAGAAAGACTCAATGCATGCCACGGAGGTGTGTATAGATGTGGGAGAGAGTTTGAGT
-----+-----+-----+-----+-----+-----+
R K T Q C M P R E V C I D V G K E F G V
-----+-----+-----+-----+-----+-----+
301 CGCGACAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGTTCCTG
-----+-----+-----+-----+-----+-----+
A T N T F F K P P C V S V Y R C G G C C

FIG. 2A

1 CGAGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCACTTACGGTCTGTCCACTGT
-----+-----+-----+-----+-----+-----+-----+
61 AGATGA~~ACT~~CATGACTGTACTCTACCAGATATTGGA~~AA~~ATGTACAAGTGTCAAGCTAAG
-----+-----+-----+-----+-----+-----+-----+
M T V L Y P E Y W K M Y K C Q L R
-----+-----+-----+-----+-----+-----+-----+
121 GAAAGAGGCTGGCAATACAGAGAACAGCCCACTCACTCAAGGACAGAGAGAC
-----+-----+-----+-----+-----+-----+-----+
K G G W Q H N R E Q A N L N S R T E E T
-----+-----+-----+-----+-----+-----+-----+
181 TATAAAATTTCCTGCAGCACATTAATAACAGAGATCTTGA~~AA~~AGTATTGATAATGAGTC
-----+-----+-----+-----+-----+-----+-----+
I K F A A A H Y N T E I L K S I D N E W
-----+-----+-----+-----+-----+-----+-----+
241 GAGAAAGACTCAATGCATGCCACGGAGGTGTGTATAGATGTGGGAAGAGATTGGAGT
-----+-----+-----+-----+-----+-----+-----+
R K T Q C M P R E V C I D V G K E F G V
-----+-----+-----+-----+-----+-----+-----+
301 CGCGACAACACCTTCTTTAAACCTCCATGTGTCTCCGTCTACAGATGTGGGGTTCCTG
-----+-----+-----+-----+-----+-----+-----+
A T N T F F K P P C V S V Y R C G G C C

FIG. 2A